

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

09/868,469  
IFW/16  
3-31-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/868/469

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1 \_\_\_\_\_ Wrapped Nucleics  
\_\_\_\_\_ Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was refiled in a word processor after creating it. Please adjust your right margin to J; this will prevent "wrapping."

2 \_\_\_\_\_ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 \_\_\_\_\_ Misaligned Amino  
\_\_\_\_\_ Numbering

The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 \_\_\_\_\_ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 \_\_\_\_\_ Variable Length

Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6 \_\_\_\_\_ PatentIn 2.0  
\_\_\_\_\_ "bug"

A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7 \_\_\_\_\_ Skipped Sequences  
(OLD RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(1) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(11) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(11) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 \_\_\_\_\_ Skipped Sequences  
(NEW RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9 \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 \_\_\_\_\_ Invalid <21>  
\_\_\_\_\_ Response

Per 1.823 of Sequence Rules, the only valid <21> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <21> response is Unknown, Artificial Sequence, or scientific name.

11 \_\_\_\_\_ Use of <220>

Use of <220> to <223> is MANDATORY if <21> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 \_\_\_\_\_ PatentIn 2.0  
\_\_\_\_\_ "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 \_\_\_\_\_ Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFW16

## RAW SEQUENCE LISTING

DATE: 03/31/2005

PATENT APPLICATION: US/09/868,469

TIME: 15:13:48

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03312005\I868469.raw

5 <110> APPLICANT: THE PENN STATE RESEARCH FOUNDATION  
 9 <120> TITLE OF INVENTION: Cyclic Peptides  
 13 <130> FILE REFERENCE: 6460-18  
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/868,469  
 C--> 17 <141> CURRENT FILING DATE: 2001-09-24  
 17 <160> NUMBER OF SEQ ID NOS: 7  
 21 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

263 <210> SEQ ID NO: 7  
 265 <211> LENGTH: 522  
 267 <212> TYPE: DNA  
 269 <213> ORGANISM: Artificial Sequence  
 273 <220> FEATURE:  
 275 <221> NAME/KEY: misc\_feature  
 277 <223> OTHER INFORMATION: PARCP2-6H  
 281 <400> SEQUENCE: 7  
 282 atggttaaag ttatcggtcg tcgttcctc ggagtgcaaa gaatatttga tattggtctt 60  
 284 cccaagacc ataattttct gctagccaat gggcgatcg ccacaattg tcatatgcac 120  
 286 caccaccacc accatggggc aggtgctgca tgcctcagtt ttggcaccga aattttaacc 180  
 288 gttgagtacg gccattgcc cattggcaaa attgtgagtg aagaaattaa ttgttctgtg 240  
 290 tacagtgttg atccagaagg gagagtttac acccaggcga tcgccaatg gcatgaccgg 300  
 292 ggagagcagg aagtattgga atatgaattg gaagatggtt cagtaatccg agctacctct 360  
 294 gaccaccgct ttttaaccac cgattatcaa ctgttggcga tcgaagaaat ttttgctagg 420  
 296 caactggact tgttgacttt agaaaatatt aagcaaactg aagaagctct tgacaaccat 480  
 298 cgttttcctt ttccattact tgacgctggg acaattaaat aa 522

E--&gt; 301 {WP213126;1}

Does Not Comply  
 Corrected Diskette Needed

(pg. 1-2) @

pls delete

09/868, 469

PAGE 2

<210> 3

<211> 14

<212> PRT

<213> Artificial Sequence

What is the source of  
Genetic material.

<220>

<221> misc\_feature

<223> CHMHGAGAA

Invalid  
response

see item # 11 on  
error summary  
sheet.

<400> 3

Cys His Met His His His His His His Gly Ala Gly Ala Ala  
1 5 10

↑  
The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## VERIFICATION SUMMARY

DATE: 03/31/2005

PATENT APPLICATION: US/09/868,469

TIME: 15:13:49

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03312005\I868469.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No  
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:301 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:527 SEQ:7  
L:301 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
L:301 M:112 C: (48) String data converted to lower case,  
L:301 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:527 SEQ:7